OFFC ☒C5

Serial Number: _O9/643 579_

ENTERED ☐ O4CO

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☑ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☑ other invalid text, such as _Extraneous material at end of file_

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

OIPE/JCWS SEP 20 2000 RECEIVED

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted _ending_ stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____

_____

_____

°Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

OIPE

```
            RAW SEQUENCE LISTING          DATE: 09/14/2000
            PATENT APPLICATION:  US/09/643,579    TIME: 16:49:22

            Input Set : A:\Cpg.pto
            Output Set: N:\CRF3\09142000\I643579.raw

            SEQUENCE LISTING
     3 (1) GENERAL INFORMATION:
C--> 5       (i) APPLICANT: RICHARD MARTIN BROGLIE
     6                      LORIN ROGER DE BONTE
     7                      WILLIAM DEAN HITZ
     8                      GUO-HUA MIAO
     9                      ROBERT STEFAN REITER
    11     (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
    12                              FATTY ACID DELTA-12
    13                              DESATURASES AND RELATED
    14                              ENZYMES FROM PLANTS
    16    (iii) NUMBER OF SEQUENCES: 17
    18     (iv) CORRESPONDENCE ADDRESS:
    19          (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
    20          (B) STREET: 1007 MARKET STREET
    21          (C) CITY: WILMINGTON
    22          (D) STATE: DELAWARE
    23          (E) COUNTRY: U.S.A.
    24          (F) ZIP: 19898
    26      (v) COMPUTER READABLE FORM:
    27          (A) MEDIUM TYPE: FLOPPY DISK
    28          (B) COMPUTER: IBM PC COMPATIBLE
    29          (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
    30          (D) SOFTWARE: MICROSOFT OFFICE 97
    32     (vi) CURRENT APPLICATION DATA:
C--> 33          (A) APPLICATION NUMBER: US/09/643,579
C--> 34          (B) FILING DATE: 22-Aug-2000
    35          (C) CLASSIFICATION:
    37    (vii) PRIOR APPLICATION DATA:
    38          (A) APPLICATION NUMBER: 08/256,047
    39          (B) FILING DATE: NOVEMBER 17, 1992
    41   (viii) ATTORNEY/AGENT INFORMATION:
    42          (A) NAME: Lynne M. Christenbury
    43          (C) REFERENCE/DOCKET NUMBER: BB-1334-A
    45     (ix) TELECOMMUNICATION INFORMATION:
    46          (A) TELEPHONE: (302) 992-5481
    47          (B) TELEFAX: (302) 892-7949
    48          (C) TELEX:
    51 (2) INFORMATION FOR SEQ ID NO: 1:
    53      (i) SEQUENCE CHARACTERISTICS:
    54          (A) LENGTH: 1464 base pairs
    55          (B) TYPE: nucleic acid
    56          (C) STRANDEDNESS: single
    57          (D) TOPOLOGY: linear
    59     (ii) MOLECULE TYPE: cDNA
    61     (ix) FEATURE:
    62          (A) NAME/KEY: CDS
```

```
                    RAW SEQUENCE LISTING            DATE: 09/14/2000
                    PATENT APPLICATION:  US/09/643,579   TIME: 16:49:22

                    Input Set : A:\Cpg.pto
                    Output Set: N:\CRF3\09142000\I643579.raw

      63          (B) LOCATION: 130..1281
C--> 65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
      67  GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGGAGACAGA GAGAGAGTTT GAGGAGGAGC    60
      69  TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCCTAC GTCAGCCAGC   120
      71  TCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC       168
      72           Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser
      73            1               5                  10
      75  AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG    216
      76  Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro
      77   15                  20                  25
      79  CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC    264
      80  Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe
      81   30              35                  40                  45
      83  AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC    312
      84  Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile
      85               50                  55                  60
      87  ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC    360
      88  Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu
      89           65                  70                  75
      91  CCT CAC GCT CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG    408
      92  Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln
      93          80                  85                  90
      95  GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC    456
      96  Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His
      97      95                  100                 105
      99  CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC    504
     100  His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile
     101  110                 115                 120                 125
     103  TTC CAC TCC TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT    552
     104  Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His
     105                  130                 135                 140
     107  CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT    600
     108  Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe
     109              145                 150                 155
     111  GTC CCC AAG AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC    648
     112  Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
     113          160                 165                 170
     115  AAC CCT TTG GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC    696
     116  Asn Pro Leu Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly
     117      175                 180                 185
     119  TGG CCT TTG TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC    744
     120  Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly
     121  190                 195                 200                 205
     123  GGC TTC GCT TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGT    792
     124  Gly Phe Ala Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg
     125                  210                 215                 220
     127  GAG CGT CTC CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC    840
     128  Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys
     129              225                 230                 235
```

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131 TAC GGT CTC TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC    888
132 Tyr Gly Leu Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val
133         240                 245                 250
135 TGC TTC TAC GGA GTT CCT CTT CTG ATT GTC AAC GGG TTC TTA GTT TTG    936
136 Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu
137         255                 260                 265
139 ATC ACT TAC TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG    984
140 Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser
141 270                 275                 280                 285
143 TCT GAG TGG GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC    1032
144 Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp
145                 290                 295                 300
147 TAC GGA ATC TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG    1080
148 Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val
149         305                 310                 315
151 GCG CAT CAC CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT    1128
152 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
153         320                 325                 330
155 ACG AAG GCG ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG    1176
156 Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly
157         335                 340                 345
159 ACG CCG GTG GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT    1224
160 Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr
161 350                 355                 360                 365
163 GTG GAA CCG GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC    1272
164 Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn
165                 370                 375                 380
167 AAT AAG TTA TGAAGCAAAG AAGAAACTGA ACCTTTCTCT TCTATGATTG           1321
168 Asn Lys Leu
170 TCTTTGTTTA AGAAGCTATG TTTCTGTTTC AATAATCTTA ATTATCCATT TTGTTGTGTT   1381
172 TTCTGACATT TTGGCTAAAA TTATGTGATG TTGGAAGTTA GTGTCTAAAA AAAAAAAAAA   1441
174 AAAAAAAAAA AAAAAAAAAA AAA                                          1464
```

176 (2) INFORMATION FOR SEQ ID NO: 2:
178   (i) SEQUENCE CHARACTERISTICS:
179   (A) LENGTH: 384 amino acids
180   (B) TYPE: amino acid
181   (D) TOPOLOGY: linear
183   (ii) MOLECULE TYPE: protein
C--> 185   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
187 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
188 1                   5                   10                  15
190 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
191                 20                  25                  30
193 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
194             35                  40                  45
196 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
197     50                  55                  60
199 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
200 65                  70                  75                  80
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RAW SEQUENCE LISTING   DATE: 09/14/2000
PATENT APPLICATION: US/09/643,579   TIME: 16:49:22

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\09142000\I643579.raw

202 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
203   85   90   95
205 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
206   100   105   110
208 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
209   115   120   125
211 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
212   130   135   140
214 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
215 145   150   155   160
217 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
218   165   170   175
220 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
221   180   185   190
223 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
224   195   200   205
226 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
227   210   215   220
229 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
230 225   230   235   240
232 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
233   245   250   255
235 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
236   260   265   270
238 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
239   275   280   285
241 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
242   290   295   300
244 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
245 305   310   315   320
247 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
248   325   330   335
250 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
251   340   345   350
253 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
254   355   360   365
256 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
257 370   375   380
259 (2) INFORMATION FOR SEQ ID NO: 3:
261   (i) SEQUENCE CHARACTERISTICS:
262.   (A) LENGTH: 1155 base pairs
263   (B) TYPE: nucleic acid
264   (C) STRANDEDNESS: single
265   (D) TOPOLOGY: linear
W--> 267   (ii) MOLECULE TYPE: DNA
269   (iii) HYPOTHETICAL: NO
271   (iv) ANTI-SENSE: NO
273   (vi) ORIGINAL SOURCE:
274   (A) ORGANISM: Brassica napus

```
                    RAW SEQUENCE LISTING              DATE: 09/14/2000
                    PATENT APPLICATION:  US/09/643,579    TIME: 16:49:22

                    Input Set : A:\Cpg.pto
                    Output Set: N:\CRF3\09142000\I643579.raw

    276    (vii) IMMEDIATE SOURCE:
    277          (B) CLONE: IMC129
    279    (ix) FEATURE:
   ·280          (D) OTHER INFORMATION: G to A transversion
    281 mutation at nucleotide 316
    282 of the D form
C--> 284    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
    286 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT    48
    287 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
    288  1               5                  10                  15
    290 GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT    96
    291 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
    292              20                  25                  30
    294 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG   144
    295 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
    296          35                  40                  45
    298 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC   192
    299 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
    300      50                  55                  60
    302 TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT   240
    303 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
    304  65                  70                  75                  80
    306 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC   288
    307 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
    308              85                  90                  95
    310 CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC   336
    311 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
    312             100                 105                 110
    314 AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC   384
    315 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
    316         115                 120                 125
    318 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC   432
    319 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
    320     130                 135                 140
    322 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG   480
    323 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
    324 145                 150                 155                 160
    326 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG   528
    327 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
    328             165                 170                 175
    330 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG   576
    331 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
    332             180                 185                 190
    334 TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT   624
    335 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
    336         195                 200                 205
    338 TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC   672
    339 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
    340     210                 215                 220
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 09/14/2000
PATENT APPLICATION: US/09/643,579   TIME: 16:49:23

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\09142000\I643579.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:284 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:972 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

OIPE

```
        RAW SEQUENCE LISTING              DATE: 09/06/2000
        PATENT APPLICATION:  US/09/643,579   TIME: 11:53:03

        Input Set : A:\BB1334A Corrected Seq Listing.txt
        Output Set: N:\CRF3\09062000\I643579.raw

            SEQUENCE LISTING
      3  (1) GENERAL INFORMATION:
C-->  5       (i) APPLICANT: RICHARD MARTIN BROGLIE
      6                      LORIN ROGER DE BONTE
      7                      WILLIAM DEAN HITZ
      8                      GUO-HUA MIAO
      9                      ROBERT STEFAN REITER
     11      (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
     12                              FATTY ACID DELTA-12
     13                              DESATURASES AND RELATED
     14                              ENZYMES FROM PLANTS
     16     (iii) NUMBER OF SEQUENCES: 17
     18      (iv) CORRESPONDENCE ADDRESS:
     19             (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
     20             (B) STREET: 1007 MARKET STREET
     21             (C) CITY: WILMINGTON
     22             (D) STATE: DELAWARE
     23             (E) COUNTRY: U.S.A.
     24             (F) ZIP: 19898
     26       (v) COMPUTER READABLE FORM:
     27             (A) MEDIUM TYPE: FLOPPY DISK
     28             (B) COMPUTER: IBM PC COMPATIBLE
     29             (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
     30             (D) SOFTWARE: MICROSOFT OFFICE 97
     32      (vi) CURRENT APPLICATION DATA:
C-->  33            (A) APPLICATION NUMBER: US/09/643,579
C-->  34            (B) FILING DATE: 22-Aug-2000
     35            (C) CLASSIFICATION:
     37     (vii) PRIOR APPLICATION DATA:
     38            (A) APPLICATION NUMBER: 08/256,047
     39            (B) FILING DATE: NOVEMBER 17, 1992
     41    (viii) ATTORNEY/AGENT INFORMATION:
     42            (A) NAME: Lynne M. Christenbury
     43            (C) REFERENCE/DOCKET NUMBER: BB-1334-A
     45      (ix) TELECOMMUNICATION INFORMATION:
     46            (A) TELEPHONE: (302) 992-5481
     47            (B) TELEFAX: (302) 892-7949
     48            (C) TELEX:


ERRORED SEQUENCES

    990  (2) INFORMATION FOR SEQ ID NO: 17:
    992       (i) SEQUENCE CHARACTERISTICS:
    993             (A) LENGTH: 5 amino acids
    994             (B) TYPE: amino acid
    995             (C) STRANDEDNESS:
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File: //C:\CRF3\Onthold\Vsr-I643579.htm

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,579

DATE: 09/06/2000
TIME: 11:53:03

Input Set : A:\BB1334A Corrected Seq Listing.txt
Output Set: N:\CRF3\09062000\I643579.raw

```
 996           (D) TOPOLOGY: linear
 998     (ii) MOLECULE TYPE: peptide
1000    (iii) HYPOTHETICAL: YES .
1002     (iv) ANTI-SENSE: NO
1004      (v) FRAGMENT TYPE: internal
1006     (ix) FEATURE:
1007           (A) NAME/KEY: Modified-site
1008           (B) LOCATION: 2
1009           (D) OTHER INFORMATION: /product= "Asp or Glu"
1011     (ix) FEATURE:
1012           (A) NAME/KEY: Modified-site
1013           (B) LOCATION: 4
1014           (D) OTHER INFORMATION: /product= "Ala or Gly"
C--> 1016     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
W--> 1018 His Xaa Cys Xaa His
     1019 1                    5
E--> 1021 17
E--> 1023 XX-XXXX
E--> 1026 17
```

Extraneous material at end of file needs to be deleted.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/643,579

DATE: 09/06/2000
TIME: 11:53:04

Input Set : A:\BB1334A Corrected Seq Listing.txt
Output Set: N:\CRF3\09062000\I643579.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:284 M:220 C: Keyword misspelled or invalid format, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:972 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1021 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1023 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1023 M:330 E: (2) Invalid Amino Acid Designator, 1
M:332 Repeated in SeqNo=17
L:1026 M:203 E: No. of Seq. differs, LENGTH:Input:5 Found:6 SEQ:17

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